

SEQUENCE LISTING

<110> Holloway, James L.
Lok, Si

<120> SECRETED PROTEIN ZACRP4

<130> 99-29

<150> 60/141,928

<151> 1999-07-01

<160> 9

<170> FastSEQ for Windows Version 3.0

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<212> DNA

<213> Homo sapiens

<220>

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ctgcagcctg	cagcccgcag	cccgcagccc	ggagccagat	cgcgggctca	gaccgaaccc	180
gactcgaccg	ccgccccccag	ccaggcgcc	atg ctg ccg	ctt ctg ctg	ggc ctg	233
			Met Leu Pro	Leu Leu Leu	Gly Leu	
			1	5		
ctg ggc cca	gcg gcc tgc	tgg gcc ctg	ggc ccg acc	ccc ggc ccg	gga	281
Leu Gly Pro	Ala Ala Cys	Trp Ala Leu	Gly Pro Thr	Pro Gly Pro	Gly	
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tcc tct gag	ctg cgc tcg	gcc ttc tcg	gcg gca cgc	acc acc ccc	ctg	329
Ser Ser Glu	Leu Arg Ser	Ala Phe Ser	Ala Ala Arg	Thr Thr Pro	Leu	
25	30		35		40	
gag ggc acg	tcg gag atg	gcg gtg acc	ttc gac aag	gtg tac gtg	aac	377
Glu Gly Thr	Ser Glu Met	Ala Val Thr	Phe Asp Lys	Val Tyr Val	Asn	

45	50	55	
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ccc ggc gcc tac ttc ttc tcc ttc acg gct ggc aag gcc ccg cac aag Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys Ala Pro His Lys 75 80 85			473
agc ctg tcg gtg atg ctg gtg cga aac cgc gac gag gtg cag gcg ctg Ser Leu Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala Leu 90 95 100			521
gcc ttc gac gag cag cgg cgg cca ggc gcg cgg cgc gca gcc agc cag Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser Gln 105 110 115 120			569
agc gcc atg ctg cag ctc gac tac ggc gac aca gtg tgg ctg cgg ctg Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg Leu 125 130 135			617
cat ggc gcc ccg cac tac gcg cta ggc gcg ccc ggc gcc acc ttc agc His Gly Ala Pro His Tyr Ala Leu Gly Ala Pro Gly Ala Thr Phe Ser 140 145 150			665
ggc tac cta gtc tac gcc gac gcc gac gct gac gcg cct gcg cgc ggg Gly Tyr Leu Val Tyr Ala Asp Ala Asp Ala Asp Ala Pro Ala Arg Gly 155 160 165			713
ccg ccc gcg ccc ccc gag ccg cgc tcg gcc ttc tcg gcg gcg cgc acg Pro Pro Ala Pro Pro Glu Pro Arg Ser Ala Phe Ser Ala Ala Arg Thr 170 175 180			761
cgc agc ttg gtg ggc tcg gac gct ggc ccc ggg ccg cgg cac caa cca Arg Ser Leu Val Gly Ser Asp Ala Gly Pro Gly Pro Arg His Gln Pro 185 190 195 200			809
ctc gcc ttc gac acc gag ttc gtc aac att ggc ggc gac ttc gac gcg Leu Ala Phe Asp Thr Glu Phe Val Asn Ile Gly Gly Asp Phe Asp Ala 205 210 215			857
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Thr Phe Asp Lys Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala
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 Thr Ala Gly Lys Ala Pro His Lys Ser Leu Ser Val Met Leu Val Arg
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 Asn Arg Asp Glu Val Gln Ala Leu Ala Phe Asp Glu Gln Arg Arg Pro
 100 105 110
 Gly Ala Arg Arg Ala Ala Ser Gln Ser Ala Met Leu Gln Leu Asp Tyr
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 Gly Asp Thr Val Trp Leu Arg Leu His Gly Ala Pro His Tyr Ala Leu
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 Gly Ala Pro Gly Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala
 145 150 155 160
 Asp Ala Asp Ala Pro Ala Arg Gly Pro Pro Ala Pro Pro Glu Pro Arg
 165 170 175
 Ser Ala Phe Ser Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala
 180 185 190
 Gly Pro Gly Pro Arg His Gln Pro Leu Ala Phe Asp Thr Glu Phe Val
 195 200 205
 Asn Ile Gly Gly Asp Phe Asp Ala Ala Ala Gly Val Phe Arg Cys Arg
 210 215 220
 Leu Pro Gly Ala Tyr Phe Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg
 225 230 235 240
 Lys Thr Leu Ser Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala
 245 250 255
 Met Ile Tyr Asp Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln
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 Ser Val Met Leu Ala Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser
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 His Asp His Asp Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile
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<223> Each Xaa is independently any amino acid residue

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<223> Xaa is asparagine or aspartic acid

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<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan or
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<221> variation
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 <223> Each N is A, T, G or C

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garggnacnw	sngaratggc	ngtnacntty	gayaargtnt	aygtnaayat	hggnggngay	180
ttygaygtng	cnacnggnca	rttymgntgy	mgngtnccng	gngcntaytt	yttywsntty	240
acngcnggna	argcnccnca	yaarwsnytn	wsngtnatgy	tngtnmgnaa	ymnggaygar	300
gtncargcny	tngcnttyga	ygarcarmgn	mgncnggng	cnmgnmgngc	ngcnwsncar	360
wsngcnatgy	tncarytnga	ytayggngay	acngtntggy	tnmgnytnca	yggngcnccn	420
caytaygcny	tnggngcncc	nggngcnacn	ttywsnggnt	ayytngtnta	ygcngaygcn	480
gaygcngayg	cnccngcnmg	nggnccnccn	gcncncncng	arccnmgnws	ngcnttywsn	540
gcngcnmgna	cnmgnwsnyt	ngtnggnwsn	gaygcnggnc	cnggnccnmg	ncaycarccn	600
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gayggngcnw	snmgnmgngm	ngaratgcar	wsncarwsng	tnatgytngc	nytnmgnmgn	840
ggngaygcng	tntggytnyt	nwsncaygay	caygayggnt	ayggngcnta	ywsnaaycay	900
ggnaartaya	thacnttyws	nggnttyytn	gtntayccng	ayytngcncc	ngcngcnccn	960
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ncttcacgct	gggcaagctg	ccgcgtaaga	cgctgtcggt	taagctgatg	aagaaccgcg	180
acgaggtgca	ggccatgatt	tacgacgacg	gcgcgtcgcg	gcgccgcgag	atgcagagcc	240
agagcgtgat	gctggccctg	cggcgcgng	acgccgtctg	gctgtcagcc	acgaccacga	300
cggctacggc	gcctacagca	accac				325

18

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<213> Artificial Sequence

<223> Oligonucleotide ZC 22168

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18

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 C1q 2 FDTEFVNIGGDFDAAAGVFERCRLPGAYFFSFTLGKLPRKTL SVKLMKNRDEVQAMIYDDG

 C1q 1 RRPGARRAASQSAMLQLDYGDTVWL
 ::
 C1q 2 ASR-RREMQSQSVMLALRRGDAVWL

Figure